

Amendments to the Claims

This listing of claims will replace all prior versions, and listings of claims in the application.

1-135. (Canceled)

136. (New) An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 50 contiguous amino acids of SEQ ID NO:4, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT
and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA
and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6
of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of
said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of
said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about
12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9
of said glycine codons are GGG.

137. (New) An isolated polynucleotide comprising a nucleic acid fragment
which encodes a polypeptide at least 90% identical to amino acids 199 to 764 of SEQ ID
NO:4, wherein said nucleic acid fragment is a variant fragment of an optimized coding
region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT
and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8
of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said
leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said
leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

138. (New) An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to amino acids 34 to 809 of SEQ ID NO:12, wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:12;

wherein about 13 of the 29 phenylalanine codons in said coding region are TTT
and about 16 of said phenylalanine codons are TTC;

wherein about 6 of the 80 leucine codons in said coding region are TTA, about 10
of said leucine codons are TTG, about 10 of said leucine codons are CTT, about 16 of
said leucine codons are CTC, about 6 of said leucine codons are CTA, and about 32 of
said leucine codons are CTG;

wherein about 26 of the 74 isoleucine codons in said coding region are ATT,
about 36 of said isoleucine codons are ATC, and about 12 of said isoleucine codons are
ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 7 of the 40 valine codons in said coding region are GTT, about 9
of said valine codons are GTG, about 5 of said valine codons are GTA, and about 19 of
said valine codons are GTG;

wherein about 10 of the 54 serine codons in said coding region are TCT, about 12
of said serine codons are TCC, about 8 of said serine codons are TCA, about 3 of said
serine codons are TCG, about 8 of said serine codons are AGT, and about 13 of said
serine codons are AGC;

wherein about 6 of the 21 proline codons in said coding region are CCT, about 7
of said proline codons are CCC, about 6 of said proline codons are CCA, and about 2 of
said proline codons are CCG;

wherein about 7 of the 28 threonine codons in said coding region are ACT, about
10 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and
about 3 of said threonine codons are ACG;

wherein about 9 of the 34 alanine codons in said coding region are GGT, about 14 of said alanine codons are GCC, about 8 of said alanine codons are GCA, and about 3 of said alanine codons are GCG;

wherein about 15 of the 35 tyrosine codons in said coding region are TAT and about 20 of said tyrosine codons are TAC;

wherein about 9 of the 21 histidine codons in said coding region are CAT and about 12 of said histidine codons are CAC;

wherein about 10 of the 41 glutamine codons in said coding region are CAA and about 31 of said glutamine codons are CAG;

wherein about 25 of the 54 asparagine codons in said coding region are AAT and about 29 of said asparagine codons are AAC;

wherein about 36 of the 86 lysine codons in said coding region are AAA and about 50 of said lysine codons are AAG;

wherein about 25 of the 55 aspartic acid codons in said coding region are GAT and about 30 of said aspartic acid codons are GAC;

wherein about 33 of the 79 glutamic acid codons in said coding region are GAA and about 46 of said glutamic acid codons are GAG;

wherein the single cysteine codon in said coding region is selected from the group consisting of TGT and TGC;

wherein the 5 tryptophan codons in said coding region are TGG;

wherein about 2 of the 27 arginine codons in said coding region are CGT, about 5 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 5 of said arginine codons are AGG; and

wherein about 6 of the 35 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 8 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

139. (New) An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to amino acids 30 to 764 of SEQ ID NO:4, wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said

serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

140. (New) The polynucleotide of claim 139, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to amino acids 30 to 764 of SEQ ID NO:4.

141. (New) The polynucleotide of claim 139, wherein the codons in said nucleic acid fragment corresponding to amino acids 192 to 197 of SEQ ID NO:4 are deleted.

142. (New) The polynucleotide of claim 141, wherein said nucleic acid fragment encodes amino acids 24 to 752 of SEQ ID NO:8.

143. (New) The polynucleotide of claim 142, which comprises nucleotides 82 to 2268 of SEQ ID NO:7.

144. (New) The polynucleotide of claim 139, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

145. (New) The polynucleotide of claim 144, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

146. (New) The polynucleotide of claim 145, wherein said heterologous polypeptide is a secretory signal peptide.

147. (New) The polynucleotide of claim 146, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

148. (New) The polynucleotide of claim 139, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

149. (New) A vector comprising the polynucleotide of claim 139.

150. (New) The vector of claim 149, which is a plasmid.

151. (New) A composition comprising the polynucleotide of claim 139, and a carrier.

152. (New) The composition of claim 151, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating agent.

153. (New) The composition of claim 152, wherein said component is selected from the group consisting of:

(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

a cytokine;

mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

a solubilized mono-phosphoryl lipid A formulation; and

CRL1005/BAK.

154. (New) The composition of claim 152, wherein said component is a cationic lipid.

155. (New) The composition of claim 154, wherein said cationic lipid is (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRIE).

156. (New) The composition of claim 152, wherein said component comprises a cationic lipid and a co-lipid.

157. (New) The composition of claim 156, wherein said co-lipid is 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE).

158. (New) The composition of claim 156, wherein said cationic lipid is (\pm) -N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRIE) and said co-lipid is 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE).

159. (New) The composition of claim 158, wherein said cationic lipid and co-lipid are in a 1:1 molar ratio.

160. (New) The composition of claim 154, wherein said cationic lipid is (\pm) -N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE).

161. (New) The composition of claim 156, wherein said component comprises (\pm) -N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a co-lipid.

162. (New) The composition of claim 161, wherein said co-lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),

1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE)

163. (New) The composition of claim 162, wherein said co-lipid is DPyPE.

164. (New) The composition of claim 151, further comprising at least one nucleic acid molecule which encodes a polypeptide selected from the group including SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID NO:16, or SEQ ID NO:40.

165. (New) The composition of claim 164, comprising SEQ ID NO:7 and SEQ ID NO:13.

166. (New) The composition of claim 153, further comprising at least one nucleic acid molecule which encodes a polypeptide selected from the group including SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID NO:16, or SEQ ID NO:40.

167. (New) The composition of claim 166, comprising SEQ ID NO:7 and SEQ ID NO:13.

168. (New) The composition of claim 154, further comprising at least one nucleic acid molecule which encodes a polypeptide selected from the group including SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID NO:16, or SEQ ID NO:40.

169. (New) The composition of claim 168, comprising SEQ ID NO:7 and SEQ ID NO:13.

170. (New) The composition of claim 158, further comprising at least one nucleic acid molecule which encodes a polypeptide selected from the group including SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID NO:16, or SEQ ID NO:40.

171. (New) The composition of claim 170, comprising SEQ ID NO:7 and SEQ ID NO:13.

172. (New) The composition of claim 163, further comprising at least one nucleic acid molecule which encodes a polypeptide selected from the group including SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID NO:16, or SEQ ID NO:40.

173. (New) The composition of claim 172, comprising SEQ ID NO:7 and SEQ ID NO:13.

174. (New) A method to treat or prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof the composition of claim 151.

175. (New) An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 50 contiguous amino acids of SEQ ID NO:12, wherein said nucleic acid fragment is a portion of an optimized coding region for the polypeptide of SEQ ID NO:12;

wherein about 13 of the 29 phenylalanine codons in said coding region are TTT
and about 16 of said phenylalanine codons are TTC;

wherein about 6 of the 80 leucine codons in said coding region are TTA, about 10
of said leucine codons are TTG, about 10 of said leucine codons are CTT, about 16 of
said leucine codons are CTC, about 6 of said leucine codons are CTA, and about 32 of
said leucine codons are CTG;

wherein about 26 of the 74 isoleucine codons in said coding region are ATT,
about 36 of said isoleucine codons are ATC, and about 12 of said isoleucine codons are
ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 7 of the 40 valine codons in said coding region are GTT, about 9
of said valine codons are GTG, about 5 of said valine codons are GTA, and about 19 of
said valine codons are GTG;

wherein about 10 of the 54 serine codons in said coding region are TCT, about 12
of said serine codons are TCC, about 8 of said serine codons are TCA, about 3 of said
serine codons are TCG, about 8 of said serine codons are AGT, and about 13 of said
serine codons are AGC;

wherein about 6 of the 21 proline codons in said coding region are CCT, about 7
of said proline codons are CCC, about 6 of said proline codons are CCA, and about 2 of
said proline codons are CCG;

wherein about 7 of the 28 threonine codons in said coding region are ACT, about
10 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and
about 3 of said threonine codons are ACG;

wherein about 9 of the 34 alanine codons in said coding region are GGT, about 14 of said alanine codons are GCC, about 8 of said alanine codons are GCA, and about 3 of said alanine codons are GCG;

wherein about 15 of the 35 tyrosine codons in said coding region are TAT and about 20 of said tyrosine codons are TAC;

wherein about 9 of the 21 histidine codons in said coding region are CAT and about 12 of said histidine codons are CAC;

wherein about 10 of the 41 glutamine codons in said coding region are CAA and about 31 of said glutamine codons are CAG;

wherein about 25 of the 54 asparagine codons in said coding region are AAT and about 29 of said asparagine codons are AAC;

wherein about 36 of the 86 lysine codons in said coding region are AAA and about 50 of said lysine codons are AAG;

wherein about 25 of the 55 aspartic acid codons in said coding region are GAT and about 30 of said aspartic acid codons are GAC;

wherein about 33 of the 79 glutamic acid codons in said coding region are GAA and about 46 of said glutamic acid codons are GAG;

wherein the single cysteine codon in said coding region is selected from the group consisting of TGT and TGC;

wherein the 5 tryptophan codons in said coding region are TGG;

wherein about 2 of the 27 arginine codons in said coding region are CGT, about 5 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 5 of said arginine codons are AGG; and

wherein about 6 of the 35 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 8 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

176. (New) The polynucleotide of claim 175, wherein said cysteine codon in said coding region is TGT.

177. (New) The polynucleotide of claim 175, wherein said cysteine codon in said coding region is TGC.

178. (New) The polynucleotide of claim 175, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:12.

179. (New) The polynucleotide of claim 178, wherein said nucleic acid fragment encodes amino acids 34 to 809 of SEQ ID NO:12.

180. (New) The polynucleotide of claim 179, wherein said nucleic acid fragment comprises nucleotides 99 to 2427 of SEQ ID NO:26.

181. (New) The polynucleotide of claim 175, wherein said nucleic acid fragment encodes amino acids 34-583 of SEQ ID NO:12.

182. (New) The polynucleotide of claim 175, wherein said nucleic acid fragment encodes amino acids 34-254 of SEQ ID NO:12.

183. (New) The polynucleotide of claim 175, wherein said nucleic acid fragment encodes amino acids 34-295 of SEQ ID NO:12.

184. (New) The polynucleotide of claim 175, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

185. (New) The polynucleotide of claim 184, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

186. (New) The polynucleotide of claim 185, wherein said heterologous polypeptide is a secretory signal peptide.

187. (New) The polynucleotide of claim 186, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

188. (New) The polynucleotide of claim 175, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

189. (New) A vector comprising the polynucleotide of claim 175.

190. (New) The vector of claim 189, which is a plasmid.

191. (New) A composition comprising the polynucleotide of claim 175, and a carrier.

192. (New) The composition of claim 191, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating agent.

193. (New) The composition of claim 192, wherein said component is selected from the group consisting of:

(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

a cytokine;

mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

a solubilized mono-phosphoryl lipid A formulation; and

CRL1005/BAK.

194. (New) The composition of claim 192, wherein said component is a cationic lipid.

195. (New) The composition of claim 194, wherein said cationic lipid is (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRIE).

196. (New) The composition of claim 192, wherein said component comprises a cationic lipid and a co-lipid.

197. (New) The composition of claim 196, wherein said co-lipid is 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE).

198. (New) The composition of claim 196, wherein said cationic lipid is (\pm)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRIE) and said co-lipid is 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE).

199. (New) The composition of claim 198, wherein said cationic lipid and co-lipid are in a 1:1 molar ratio.

200. (New) The composition of claim 194, wherein said cationic lipid is (\pm)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE).

201. (New) The composition of claim 196, wherein said component comprises (\pm)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a co-lipid.

202. (New) The composition of claim 201, wherein said co-lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),

1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE)

203. (New) The composition of claim 202, wherein said co-lipid is DPyPE.

204. (New) The composition of claim 191, further comprising at least one nucleic acid molecule which encodes a polypeptide selected from the group including SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID NO:16, or SEQ ID NO:40.

205. (New) The composition of claim 204, comprising SEQ ID NO:7 and SEQ ID NO:13.

206. (New) The composition of claim 193, further comprising at least one nucleic acid molecule which encodes a polypeptide selected from the group including SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID NO:16, or SEQ ID NO:40.

207. (New) The composition of claim 206, comprising SEQ ID NO:7 and SEQ ID NO:13.

208. (New) The composition of claim 194, further comprising at least one nucleic acid molecule which encodes a polypeptide selected from the group including SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID NO:16, or SEQ ID NO:40.

209. (New) The composition of claim 208, comprising SEQ ID NO:7 and
SEQ ID NO:13.

210. (New) The composition of claim 198, further comprising at least one
nucleic acid molecule which encodes a polypeptide selected from the group including
SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID
NO:16, or SEQ ID NO:40.

211. (New) The composition of claim 210, comprising SEQ ID NO:7 and
SEQ ID NO:13.

212. (New) The composition of claim 203, further comprising at least one
nucleic acid molecule which encodes a polypeptide selected from the group including
SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO: 10, SEQ ID NO:14, SEQ ID
NO:16, or SEQ ID NO:40.

213. (New) The composition of claim 212, comprising SEQ ID NO:7 and
SEQ ID NO:13.

214. (New) A method to treat or prevent anthrax infection in a vertebrate
comprising: administering to a vertebrate in need thereof the composition of claim 191.